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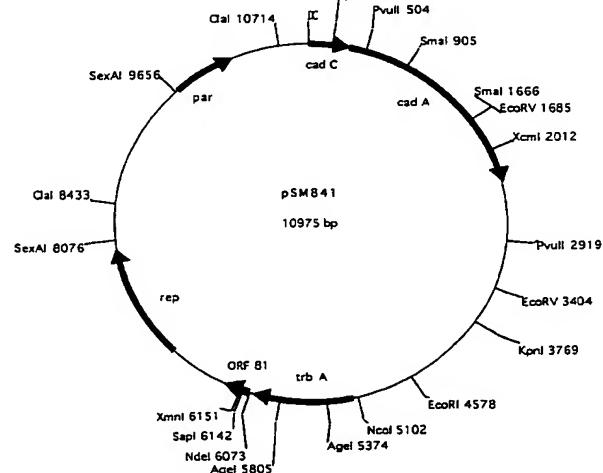
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(54) **Means and methods for the expression of homologous and heterologous proteins in strains of Rhodococcus**

(57) A description follows of a plasmid vector of Rhodococcus, a new constitutive promoter, an expression vector containing said promoter and microorganisms transformed with the expression vector. The ex-

pression vector has a high stability in the absence of selective pressure in the transformed strains of Rhodococcus and is particularly useful for the production of proteins of interest.

Fig.1



Description

[0001] The present invention relates to a plasmid vector of Rhodococcus, a new constitutive promoter, an expression vector containing said promoter, microorganisms transformed with the expression vector and their use in the production of proteins.

[0002] Bacteria of the Rhodococcus genus are of wide interest in the field of the biodegradation and biotransformation of organic compounds (Warhurst and Fewson, 1994, Crit. Rev. Biotechnol., 14:29-73).

[0003] Processes are known, for example, which use strains of Rhodococcus for the selective removal of organic sulfur from fossil fuels (U.S. 5,358,870, U.S. 5,132,219, PCT/US92/01868, EP-445896) and for the production of enzymes involved in the production of acrylamides (Kobayashi et al., 1992, Trends Biotechnol., 10:402-408), carboxylic acids, L-aminoacids (W09804733) and enantiomorphs of chiral compounds (U.S. 5,672,504).

[0004] The main restricting factor in optimizing biocatalysis processes which use these bacteria is however the lack of suitable genetic instruments.

[0005] This term refers to expression vectors in Rhodococcus which:

- are present in cells in multiple copies;
- are steadily maintained inside the cells without costly selective agents (for example antibiotics), which considerably influence the economic convenience of an industrial process; and
- contain a strong promoter, i.e. capable of allowing an effective expression of a gene, or a strong constitutive promoter which does not require the use of inductors and is not susceptible to repressors.

[0006] In fact, a limit in the removal of organic sulfur from fossil fuels with strains of Rhodococcus which produce the sox enzymatic complex, is due to the presence, upstream the corresponding genes, of a promoter greatly inhibited by sulfate.

[0007] To overcome this drawback, the genes encoding this enzymatic complex were placed in Rhodococcus vectors under the control of constitutive heterologous promoters such as that of the gene for resistance to chloramphenicol of Rhodococcus fascians (Piddington, C.S. et al., 1995, Appl. and Env. Microbiol., 61,2,: 468-475) or of the gene sacB of B.subtilis (Denis-Larose, C. et al, 1998, Appl. and Env. Microbiol., 64,11,:4363-4367) and of the gene for resistance to Kanamycin of E.coli (Serbolisca et al., Appl. Microbiol. Biotechnol. 1999, 52:122-126). The maintenance of the vectors, however, required the presence of a selective agent in the culture medium and, furthermore, the expression of the sox operon under the control of the promoter sac B proved to be very low (Lau. P. et al. 1999 ACS Fuel Chem.: 32-33).

[0008] It has now been found that the disadvantages of the known art described above can be overcome by the expression vector of the present invention.

[0009] In accordance with this, a first objective of the present invention relates to the cloning plasmid vector pSM843 stable in Rhodococcus.

[0010] A further objective of the present invention relates to a new constitutive promoter of Rhodococcus capable of directing the expression of a homologous or heterologous gene with a high efficiency and characterized by the sequence SEQ. ID. Nr. 2.

[0011] Another objective of the present invention relates to an expression vector in Rhodococcus which comprises said constitutive promoter.

[0012] A further objective of the present invention relates to a strain of Rhodococcus transformed with said expression vector.

[0013] Yet another objective of the present invention relates to a process for the production of homologous or heterologous proteins in Rhodococcus bacteria transformed with said expression vector.

[0014] Additional objectives of the present invention will appear evident from the following description and examples.

Brief description of the figures

[0015] Figure 1: shows the restriction map of the 11 kb plasmid pSM841.

[0016] Figure 2: shows the restriction map of the 7.3 kb plasmid pSM843.

[0017] Figure 3: shows the restriction map of the E.coli plasmid pSM839.

[0018] Figure 4: shows the restriction map of the plasmid pSM846. Figure 5: shows the restriction map of the plasmid pSM847.

[0019] In particular, the expression vector according to the present invention comprises:

- (a) the rep genes, ORF81 and trbA which encode proteins involved in replication in Rhodococcus;
- (b) a gene called parA whose product is necessary for maintaining the plasmid in the absence of selective pressure

and is characterized by the sequence SEQ ID. Nr. 1;
 (c) a constitutive promoter of Rhodococcus having the sequence SEQ. ID. Nr. 2;
 (d) a multiple cloning site downstream the promoter; and
 (e) at least one gene which encodes a genetic marker selected, for example, from genes of the cad operon (SEQ. ID. Nr. 3), which provide resistance to cadmium or genes which encode resistance to an antibiotic.

5 [0020] The expression vector also contains the replication origin in E.coli and can therefore be used as shuttle vector in Rhodococcus and E.coli.

10 [0021] The expression vector, indicated hereunder as pSM846, was obtained by:

- (1) construction of the cloning vector pSM843;
- (2) isolation of a constitutive promoter of Rhodococcus; and
- (3) insertion of said constitutive promoter into the vector pSM843.

15 [0022] The plasmid vector pSM843 was prepared by reducing the dimensions of the 130 kb plasmid of Rhodococcus sp. DS7 containing the sox operon, the genes which confer resistance to cadmium, and those for resistance to arsenic (Margarit et al., 1997 and Serbolisca et al., 1999). This reduction was effected by means of the following strategy:

- (a) search for plasmids deriving from the deletion of the 130 kb plasmid following transformation of a recipient strain and isolation of a 22 kb plasmid;
- (b) digestion of said plasmid with suitable restriction enzymes, self-ligase and isolation of the 11 kb plasmid pSM841;
- (c) characterization of the plasmid obtained in (b) and
- (d) construction of the 7.3 kb plasmid pSM843 containing at least one genetic marker and the genes parA, rep and trbA respectively necessary for stability and replication in Rhodococcus.

20 [0023] The stability of the vectors obtained was controlled after each reduction so as to select only those maintained in at least 90% of the cells of the host strain for at least 30-40 generations, in complete medium and in the absence of selective pressure.

25 [0024] Research on constitutive promoters inside the chromosome of a strain of Rhodococcus was effected for the construction of the expression vector, using a new method, which is included in the scope of the present invention.

30 [0025] This method is based on the observation that strains of Rhodococcus have the capacity of integrating at random fragments of foreign DNA in their chromosome, without the necessity for a sequence homology higher than 3 bp between the donor DNA and that of the host. The integration effectiveness was estimated at about 10^2 - 10^3 colonies per μ g of DNA in Rhodococcus transformation experiments.

35 [0026] The method consists in:

- (i) transforming a strain of Rhodococcus directly with a gene reporter without its promoter or with a multicopy plasmid of E.coli containing said gene and linearized upstream the gene reporter;
- (ii) selecting the clones which express said gene, i.e. the clones which have integrated the gene reporter in their chromosome, downstream a promoter sequence;
- (iii) digesting the chromosomal DNA of the selected clones with restriction enzymes which cut upstream and downstream the gene;
- (iv) amplifying the DNA obtained in step (iii); and
- (v) sequencing the promoter upstream the gene reporter.

40 [0027] Gene reporter refers to a fragment of DNA which encodes a product that allows the selection of the clones which express it. Examples of gene reporters useful for this purpose can be selected from those which encode resistance to antibiotics or heavy metals or enzymes such as XylE or the same Sox proteins.

45 [0028] With respect to the techniques currently used, this method is much more efficient and rapid as it does not require the preparation of genome banks with fragments of chromosomal DNA upstream the gene reporter. This method can be applied to all microorganisms which, like Rhodococcus, are capable of integrating at random fragments of foreign DNA in their chromosome without the necessity for a high sequence homology between the donor DNA and that of the host.

50 [0029] With this method, a constitutive promoter was identified of a gene of Rhodococcus having the sequence SEQ. ID Nr. 2. This promoter was inserted into the plasmid vector pSM843, obtaining the expression vector pSM846 which can be used for the production of proteins of interest in Rhodococcus.

55 [0030] The segregational and structural stability of the expression vector pSM846 in strains of Rhodococcus was

determined by operating as described in Example 4. The results demonstrated that the vector is maintained in over 90% of the cellular population even after subsequent culture passages without selective agents, thus showing a high segregational stability.

[0031] Furthermore, analysis of the plasmids isolated from the transformed strains showed that, even after various generations in liquid culture, this plasmid remains structurally stable in different strains of Rhodococcus with from 4 to 8 copies per cell.

[0032] The expression vector of the present invention can be used for the expression of genes which encode proteins of interest such as, for example, enzymes involved in the selective removal of organic sulfur from fossil fuels (SoxA, SoxB, SoxC, SoxD), the production of L-aminoacids (amidase, aspartase), the production of enantiomorphs of chiral compounds (epoxide hydrolase, ketoesteroreductase), the production of carboxylic acids (nitrilase), etc.

[0033] The expression vector can be used in various species of Rhodococcus and in phylogenetically similar bacteria such as Gordona and Nocardia.

[0034] The capacity of the promoter of directing the constitutive expression of the gene put under its control was verified by positioning downstream said promoter, the sox operon isolated according to what is described by Serbolisca, L., de Ferra, F., Margarit, I., Appl. Microbiol. Biotechnol., 1999, 52:122-126.

[0035] The results obtained demonstrated that this promoter allows an effective and constitutive expression of the SoxA, SoxB and SoxC proteins in the presence of inorganic sulfur in the culture medium.

[0036] The strains containing the vectors pSM843, pSM846 and pSM847 were deposited at the Centraalbureau Voor Schimmel-cultures as Rhodococcus SMV 112, SMV 113 and SMV 114, where they received the respective numbers CBS 102445, 102446 and 102447.

[0037] The following were used in the experiments described hereunder:

- the 130 Kb plasmid containing the sox operon which encodes enzymes responsible for the conversion of dibenzothiophene (DTB) to 2-hydroxybiphenyl, and the genes which encode resistance to cadmium and arsenic. Said plasmid was isolated from the strain Rhodococcus sp. DS7 (Margarit, I. et al., 1997, 9th Proceedings of the International Conference on Coal Science: 1579-1582);
- the plasmid pSM789, incapable of replicating itself in Rhodococcus, obtained by inserting into the plasmid of E. coli pUC18, the 4549 bp fragment HindIII-EcoRI which contains the sox operon without promoter isolated from Rhodococcus sp. DS7 (Margarit, I. et al., 1997, 9th Proceedings of the International Conference on Coal Science: 1579-1582).

[0038] The Rhodococcus sp. DS7 strain was previously classified as Arthrobacter on the basis of microbiological test (D'Addario 1996 Proceedings of the Symposium AAA Biotechnology. Shejbal, E. and Ferrara: 139-149). Subsequently, a comparison of the DNA 16 S sequence with that of the data banks indicated that the strain belonged to the Rhodococcus genus. The most consistent homologies were found with Rhodococcus erythreus and Rhodococcus erythropolis.

[0039] The following examples are illustrative but do not limit the scope of the invention itself.

EXAMPLE 1

Construction of the plasmid vector pSM843

[0040] Electrocompetent cells of Rhodococcus DS-2 (100 µl) (BIORAD Gene Pulser TM, 400 ohm, 25 uF) were transformed with the 130 kb plasmid (100 ng). The recombinant clones were selected on plates of LB-agar containing 0.5 mM of CdCl₂ and subsequently plated on minimum medium (10 g/l of KH₂PO₄ pH 7.4, 2.5 g/l of NH₄Cl, 0.2 g/l of MgCl₂·6H₂O, 0.02 g/l of CaCl₂, 0.01 g/l of FeCl₃, 0.005 g/l of MnCl₂·2H₂O, 0.003 g/l of ZnCl₂, 0.0009 g/l of CuCl₂·2H₂O, agarose 0.8%) containing dibenzothiophene (DBT) as sole sulfur source. One of the cadmium-resistant clones proved to be incapable of desulfurizing DBT. The plasmid DNA was extracted from this clone, which, after being tested on agarose gel at 0.7%, showed dimensions of about 100 kb.

[0041] Operating as described above, from the transformation of DS-2 with the 100 kb plasmid, a 35 kb plasmid was obtained which no longer conferred resistance to arsenic, and from this a 22 kb plasmid.

[0042] The plasmid stability was checked for the three vectors in order to select only those maintained in the host strain for at least 30-40 generations in the absence of selective pressure.

[0043] The 22 kb plasmid (1 µg) was digested with 4 U of the restriction enzyme *Sex A1* (Boehringer), in 10 µl of the salts supplied by the producer, incubating for 60 minutes at 37°C and 15 minutes at 70°C. The linearized plasmid (2 µl) was self-ligated in 10 µl of buffer, in the presence of 1 U of *T4 DNA ligase*, for 16 hours at 16°C. 1 µl of the ligase mixture was used to transform DS-2 electrocompetent cells. A 18.7 kb plasmid was isolated from one of the clones containing plasmids with reduced dimensions. This plasmid was digested with the enzyme *EcoRI* obtaining a 15.8 kb vector which was further reduced by digestion with the enzymes *SspI* and *DraI*, which leave truncated ends.

[0044] The resulting 11 kb plasmid, called pSM841 (figure 1), was sequenced and showed the presence of:

- the *cad* operon which confers resistance to cadmium and having the sequence SEQ. ID. Nr. 3;
- *rep* genes, *ORF81* and *trbA* encoding proteins involved in replication described by Denis-Larose, C. et al., 1998, *Appl. and Env. Microbiol.*, **64**, 11: 4363-4367. A 15 bp sequence was identified between these two genes, which, by homology with other sequences, may correspond to the replication origin of the plasmid; and
- a gene *parA* whose sequence (SEQ ID Nr. 1) shows a partial homology with that of genes involved in the partitioning of the plasmids which takes place during the cellular division. 2 repeated sequences each of 24 bp, were identified upstream this gene.

[0045] To confirm the importance of the DNA region containing the *parA* gene in maintaining pSM841, an 8.8 kb plasmid was constructed without this region. The results demonstrated a reduction of over 50% in the plasmid stability.

[0046] Once the genes indispensable for maintaining the plasmid pSM841 had been identified, a 7.3 kb vector was constructed, containing:

- 1- a fragment *DraI-EcoRI* of 2717 bp comprising the *cad* operon;
- 2- a fragment *SspI-NcoI* of 2716 bp comprising the genes *trb A* and *rep A*;
- 3- a fragment *EcoRI-NcoI* of 1857 bp comprising the gene *par A* and a multiple cloning site (MCS).

[0047] These fragments were isolated from the plasmid pSM841 by means of amplification and then ligated in the presence of *T4 DNA ligase* at 16°C for a night.

[0048] The resulting plasmid, called pSM843, has the restriction map indicated in figure 2.

EXAMPLE 2

Isolation of the constitutive promoter

[0049] The plasmid pSM789 (5 µg) was digested with 40 Units (U) of the restriction enzyme *HindIII* (Boehringer) in 50 µl of buffer supplied by the manufacturer.

[0050] After incubation at 37°C for 60 minutes the denaturation/extraction of the proteins was effected by adding a volume of phenol-chloroform (1:1) and a volume of chloroform:isoamyl alcohol (23:1). The DNA was subsequently precipitated by adding 5 µl of a 3 M solution of Na-acetate and 300 µl of ethanol to the aqueous phase and then resuspended in 10 µl of H₂O. In this way, an open linear plasmid was obtained exactly upstream the RBS region of the first gene of the *sox* operon (*sox A*).

[0051] The linearized DNA (0.2 µg) was used to transform 100 µl of cells of *Rhodococcus* sp. DS-2 and the transformants were then selected on minimum medium plates containing 0.04 g/l of DBT and 1% of C₂H₅OH as sole sources of sulfur and carbon, respectively.

[0052] 100 clones capable of growing were isolated using DBT. As the plasmid pSM789 was incapable of replicating itself in *Rhodococcus*, the transformants obtained (about 10² per µg of DNA used) had to contain the *sox* operon inside their chromosome, downstream a promoter which allowed its expression.

[0053] In order to determine whether the integration took place in different points of the chromosome, the chromosomal DNA was extracted from 20 clones (Current Protocols in Molecular Biology - Vol 1) and digested with 20 U of the enzyme *NotI*, for which there is only one binding sequence inside the *sox* operon. The digested DNA was subjected to electrophoresis on agarose gel 0.8%, visualized by colouring with EtBr 0.5% and transferred onto nylon (Nylon Membranes, positively charged - Boehringer) by means of Southern Blot (Sambrook, J., Fritsch, E.F., Maniatis, T. 1989 Molecular cloning: a laboratory manual 2nd edn. Cold Spring Harbor, NY).

[0054] The DNA was then hybridized with a probe whose nucleotidic sequence corresponded to a fragment of 770 bp of the *sox C* gene, using the non-radioactive method provided by the DIG SYSTEM- kit Boehringer. The hybridization reaction was effected at 68°C.

[0055] Of the clones tested a single band was observed, with a different molecular weight for each clone, which indicated a single integration event of the plasmid pSM789 in different points of the chromosome.

[0056] In order to verify if these clones were capable of desulfurizing DBT in the presence of inorganic sulfur, they

were plated on minimum medium containing both DBT and $MgSO_4 \cdot 7H_2O$ (0.20 g/l), in parallel with the *Rhodococcus* sp. DS7 strain. After 12 hours, upon exposing the plate to UV rays at 254 nm, a fluorescent halo was observed for all the recombinant clones, whereas no halo was visible for the native strain. This indicated that the activity of the isolated promoters was not repressed by sulfate. The clone which had the most consistent halo was called SMV110.

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EXAMPLE 3

Characterization of the promoter contained in SMV110

10 [0057] 1 μ g of chromosomal DNA of the clone SMV110 was digested with 20 U of the enzyme *Clal*, in 10 μ l of buffer (Boehringer), at 37°C for 16 hours. After deactivation of the enzymes at 70°C for 15 minutes, 2 μ l of the digested DNA was treated with 1 U of the enzyme T4 DNA ligase in 10 μ l of buffer (Boehringer), incubating at 16°C for 16 hours.

[0058] An aliquot (1 μ l) of the ligase mixture was used to transform cells of *E.coli* XL1-Blue made electrocompetent (Dower, W.J. et al. 1988 Nucleic Acids Research, 16: 6127-6145).

15 [0059] The transformants were selected on plates of agarized LB medium containing 100 μ g/ml of Ampicillin. The plasmid DNA extracted from one of the clones thus obtained was analyzed by restriction analysis. The results indicated that the plasmid consisted of a 4.5 kb fragment, deriving from the chromosomal DNA of DS-2, and the plasmid pSM789. The map of this new plasmid, called pSM839, is showed in figure 3.

20 [0060] The 4.5 kb fragment was then amplified with the Polymerase Chain Reaction (PCR) technique, (Leung, D. W., Chen, E., Goeddel, D.V., 1989 Technique- a journal methods in cell and molecular biology, 1, Nr. 1: 11-15), using the following pair of oligonucleotides:

25 1) 5' CAGTCACGAC GTTGTAAAAC GA 3' (FORWARD)

30 2) 5' TGCATTTGTC GTTGTGAGT 3' (REVERSE)

35 [0061] The amplification was carried out in a DNA Thermal Cycler 480 apparatus (Perkin-Elmer Cetus) using 100 μ l of a reaction mixture containing: 5 ng of plasmid DNA, 60 pmoles of the two oligonucleotides, 200 μ M of dNTPs (dATP, dGTP, dTTP, dCTP) and 1 U of *Taq* polymerase (Boehringer), in the buffer recommended by the manufacturer. After denaturation for 2 minutes at 94°C, the cyclic program was started, which comprises: 1 minute at 98°C, 1 minute at 60°C and 3 minutes at 72°C for a total of 25 cycles, followed by 8 minutes at 72°C (final extension).

[0062] The amplified 4.5 kb fragment was then sequenced by means of a DNA sequencer ABI 373 (Perkin Elmer). The sequence and possible open reading frames were compared with those present in DNA and protein banks using the research motor BLAST supplied by NCBI (Altschul, S.F., Madden, Th, Schaffer, A., Zhang, J., Zhang, Z., Miller, W., Lipman, D., 1997 Nucleic Acids Research 25: 3398-3402).

40 [0063] The results showed that the integration of pSM789 in the chromosomal DNA of the DS-2 strain had taken place inside a gene which encodes a protein homologous to some endoglucanases and amylases of other microorganisms.

[0064] It was therefore deduced that in the clone SMV110, the expression of the *sox* operon was controlled by the promoter of said gene. In order to characterize this promoter, the exact transcription starting point of the *sox* operon was determined by primer extension using the 5' RACE System kit (BRL).

45 [0065] The results indicated that the start of the transcription of the *sox* operon took place at a distance of 622 bp from 5' of the operon and that the promoter was therefore situated immediately upstream said region.

[0066] Analysis of the sequence upstream the transcription starting site revealed the presence of the presumed -10 region.

50

EXAMPLE 4

Construction of the expression vector pSM846

55 [0067] A 1100 bp fragment containing the constitutive promoter was amplified by PCR starting from the plasmid pSM839 using the following oligonucleotides:

(i) 5' GATCGGCCGGG ATCCACGAGT GTT 3' (forward)

5 BamHI

(ii) 5' ACCAACACT GA GCTGTTAA CGGCCGGAGC GGCGATGCA

10 HindIII HpaI SfiI

TTTTAGGTGA TGCCCGGG 3' (reverse) .

15 Nsi

[0068] The amplified fragment was digested with the enzymes HindIII and BamHI, eluted from agarose and inserted into the plasmid pUC18. The resulting plasmid was digested with the enzymes AfI_{III}-HpaI and ligated to pSM843, previously digested with AfI_{III} and Ncol (which form compatible ends with the former) in the presence of T4 DNA ligase at 16°C for a night. A new vector shuttle of E.coli-Rhodococcus, called pSM846, was thus obtained, containing the promoter followed by an MCS for the constitutive expression of proteins in Rhodococcus. The strain of Rhodococcus DS-2 containing the plasmid pSM846, whose map is showed in figure 4, was called SMV112.

25 EXAMPLE 5

[0069] In order to verify the stability of the plasmid pSM846 in the transformed strains of Rhodococcus after a prolonged period of culture in the absence of selective pressure, three independent clones of the strain SMV112 were grown at 30°C, 200 rpm for 16 hours in 100 ml flasks, containing 20 ml of LB medium (Bacto Tryptone 10 g/l, yeast extract 5 g/l, NaCl 10 g/l).

[0070] The three cultures (0.1 ml) were used to inoculate a further 20 ml of the same mediums, and the new cultures were grown at 30°C, 200 rpm for 16 hours. This procedure was repeated a further 3 times, the cellular growth being followed as an increase of the optic density measured at 600 nm (O.D. 600).

[0071] At the end of each growth, aliquots of cultures were removed, suitably diluted and then plated on LB agar medium. The plates were incubated at 30°C for 16 hours and the colonies were then counted (CFU/ml). In this way it was determined that there were at least 35 generations at the end of the experiment.

[0072] In order to determine the percentage of cells which had maintained the plasmid for at least 35 generations, and were therefore resistant to cadmium, 100 single colonies deriving from the plating by dilution, after the 5th growth of the three cultures, were placed on LB plates containing CdCl₂ at a concentration of 0.5 mM.

[0073] It was observed that the plasmid was maintained in over 90% of the cellular population, thus showing a considerable segregational stability even after subsequent passages in culture in the absence of selective pressure.

[0074] In order to verify the structural stability of the plasmid pSM846, at the end of the 5th growth passage, the plasmid DNA was extracted from an aliquot of the cultures of 12 clones, using the method described in Serbolisca et al. (1999). The DNA obtained were digested with various restriction enzymes for which there are single or double sites in the plasmid pSM846 and analyzed by means of electrophoresis on agarose gel for 2 hours at 90 V, 90 mA; the gels were coloured with Ethidium Bromide 1 mg/ml. The visualization of the gel on a UV light trans-illuminator showed the expected bands according to the restriction map of the plasmid, demonstrating that pSM846 was structurally stable in Rhodococcus for several generations in the absence of selective pressure.

50 EXAMPLE 6

Determination of the number of copies of pSM846 per cell

[0075] The average number of copies of the plasmid pSM846 per cell was estimated by means of quantitative PCR on preparations of total DNA from cells of Rhodococcus DS-2 containing said plasmid. The method is based on the determination of the quantity of DNA obtained by amplification of a fragment of the plasmid. This quantity is directly correlated to the concentration of the plasmid itself, used as a mould in the amplification reaction.

[0076] The total DNA was prepared according to the method illustrated in Current Protocols in Molecular Biology -

Ausubel et al., Ed. Wiley Interscience Section 2.4.1 with the following modification: to obtain a complete cellular lysis the centrifuged cells from 1.5 ml of culture were resuspended in 567 microliters of TE (TrisHCl 10 mM, EDTA 1 mM, pH 8) containing lysozyme 50 µg/ml and were incubated at 37°C for 20 minutes before adding SDS and proteinase K according to protocol.

5 [0077] After a treatment of 10 minutes with RNasi, the concentration of total DNA was estimated on agarose gel and the samples were diluted to 100 pg of DNA per microliter.

[0078] PCR reactions were effected on the DNA thus obtained, using two oligonucleotides (primers) which appear inside the operon for resistance to cadmium and having the following sequence:

10 - 5' TGGCCCGGCC GGAATTGATG GAC 3' (primer Cd4)

and

15 - 5' GCCGACGGCC GCGATCGTGA TCAG 3' (primer Cd17).

20 [0079] The standardization was effected by means of a second PCR reaction on the portion of chromosomal DNA encoding RNA 16S of Rhodococcus DS7 using oligonucleotides specific for this sequence.

[0080] The number of copies of plasmid was estimated on both the strain containing the plasmid pSM846 and on a strain containing a single copy of the genes for resistance to cadmium integrated in the chromosome and on the strain DS7.

25 [0081] The amplification reactions were carried out according to the instructions of the Syber Green kit of Perkin Elmer-AB.

[0082] The amplified DNA was marked with the Syber Green fluorescent marker and quantified with a PE Applied Biosystems GeneAmp 5700 instrument. Each sample was triply amplified and the fluorescence values were compared with calibration curves included in each experiment for each pair of primers. The quantity of DNA obtained by amplifying with the primers specific for the plasmid was then corrected for the quantity of chromosomal DNA amplified with the primers specific for the RNA 16S genes.

30 [0083] On comparing the three strains tested it was established that the strain DS7 contains an average of 2-3 copies of the 130 kb plasmid per cell, whereas cells of Rhodococcus DS-2 transformed with pSM846 contain from 4 to 8 copies of plasmid per cell.

35 EXAMPLE 7

Construction of the plasmid pSM847

40 [0084] The objective of the experiment was to obtain a strain containing several copies of sox genes under the control of the constitutive promoter identified.

[0085] The fragment of DNA containing the promoter identified in example 3, was amplified starting from the plasmid pSM839 by means of PCR, using the following oligonucleotides:

45 - 5' ATTCGAGAGT GCATATGCGG AAC 3' (FORWARD)

50 - 5' CCATTTCTTC CAAGCTTCCG CCG 3' (REVERSE)

which pair with the sequence SEQ. ID. Nr. 2, into which the restriction sites NdeI and HindIII were introduced.

[0086] About 500 ng of the DNA obtained from the amplification reaction were digested with 4 U of the enzymes NdeI and HindIII for 60 minutes at 37°C and purified on Nusieve agarose gel at 1.5% (FMC products). Parallelly, 1 µg of the plasmid pSM789 was digested with 4 U of the same enzymes for 60 minutes at 37°C. 50 ng of vector and 25 ng of insert purified from agarose were then ligated in the presence of 1 U of the enzyme T4 ligase. The ligase mixture was subsequently used to transform competent cells of E.coli XL-blue.

[0087] 500 ng of the plasmid extracted from one of the clones of E.coli containing the desired insert, and 500 ng of the plasmid pSM843 were digested separately with 4 U of the restriction enzyme SspI (New England Biolabs). The

reactions were carried out at 37°C for 60 minutes and at 70°C for 10 minutes.

[0088] 150 ng of the linear plasmid pSM843 were then ligated with 50 ng of the plasmid of *E.coli* in 10 µl of buffer (Boehringer), in the presence of 1 U of T4 DNA ligase, incubating for 16 hours at 16°C. 1 µl of the ligase mixture was used to transform electrocompetent cells of *Rhodococcus* DS-2. The cells were plated on minimum medium in the presence of DBT and cultivated at 37°C for 4-5 days.

[0089] The plasmid DNA was extracted from one of the colonies thus obtained, according to the method described in Serbolisca et al. (1999, Appl. Env. Microbiol. 52:122-126) and subjected to restriction analysis with enzymes for which there are sites in the starting plasmids. The vector thus obtained, containing the sox operon under the control of the constitutive promoter, was called pSM847 (Figure 5) and the strain containing it SMV114.

EXAMPLE 8

[0090] The strain SMV114 was cultivated in parallel with the strain *Rhodococcus* DS7 in minimum medium plus DBT with and without 0.20 g/l of MgSO₄·7H₂O.

[0091] Electrophoresis and Western blot analysis of the soluble proteins extracted from the bacterial cultures showed that:

1. when the strains are grown in DBT without sulfate, SMV114 expresses higher quantities of Sox A, B and C proteins than DS7;
2. in the presence of inorganic sulfate, the strain *Rhodococcus* DS7 does not express the Sox enzymes, whereas SMV114 expresses the same quantity of enzymes with respect to growth without sulfate.

[0092] The desulfurizing activity of the strain SMV114 was measured on resting cells using DBT as substrate and compared with that of the strain *Rhodococcus* sp. DS7. From a pre-inoculum in minimum medium, two inocula were effected for each strain in 100 ml of the same medium, without and with inorganic sulfur (0.20 g/l of MgSO₄·7H₂O, 80 mM). The growths were effected for 20 hours at 30°C in flasks with breakwater protection. The starting optical density, measured at 660 nm, was OD 0.25 for the cultures in MgSO₄ + DBT and 0.4 for the cultures with DBT alone. The dry weight was triply determined, from 5 ml of centrifuged culture at 5000-6000 rpm for 10 minutes, frozen at -80°C and lyophilized.

[0093] For the measurement of the desulfurizing activity, 10 ml of culture were removed and centrifuged at 5000-6000 rpm for 10 minutes, at room temperature. The cells were resuspended in 9.75 ml of Tris-HCl 20 mM pH 7, introduced into 50 ml flasks and incubated in a stirred bath at 30°C for 5 minutes. After adding 250 µl of DBT 40 mM to the suspension, a first sampling (1 ml) was effected immediately, which was extracted with 2 ml of ethyl acetate, to determine the product background at time zero. Subsequent samples were taken after 1 and 2 hours.

[0094] 20 µl of the clarified organic phase were analyzed by HPLC on a chromatographic column in C18 Vydac type TP218-5418 inverse phase, with a program comprising a flow of 1 ml/min for 15 minutes in 80% of acetonitrile. The specific activity, expressed as mg of 2HBP produced per hour per gram of dry weight, was calculated from the area corresponding to the product 2-hydroxybiphenyl (2 HBP) and taking in account the dry weight.

[0095] The activity values obtained without inorganic sulfur corresponded to 5 +/- 0.6 mg/h.g both for the native strain and for SMV114. When cultivated in the presence of 0.2 g/l of MgSO₄, the *Rhodococcus* DS7 strain did not express any desulfurizing activity, whereas the SMV114 strain maintained its activity.

EXAMPLE 9

[0096] The possibility of using the plasmid pSM847 in other species of *Rhodococcus* was also examined. 100 ng of the plasmid were used to transform electrocompetent cells of strains of *Rhodococcus erythropolis*, *Rhodococcus rhodochrous* and *Rhodococcus opacus*. In all cases colonies capable of desulfurizing DBT were obtained, which contained the plasmid having the estimated dimensions. Also in this case, at least 90% of the clones maintained the plasmid for about 40 generations in the absence of selective pressure.

50

55

SEQUENCE LISTING5 SEQ ID NO: 1

SEQUENCE TYPE: Nucleotide

SEQUENCE LENGTH: 2290 base pairs

10 STRANDEDNESS: Single

TOPOLOGY: Linear

15 ATCGATTTTT CCGCCGGCGG CGCCGCCGCA TCCCACGCTG CCGTGAGTCC 50

GTCCAAAGCT CGCAGCATCG ACGGGTGGTA CTTACGCAAC GCTGCCTGGC 100

20 TGAACCCGGC GTTGAGGATG ATGTGCGCCT TCTGCCAGTT GGGTTCGGAG 150

TTGAAAGCGG TGAAAAGGCC GTCCCTCCGCG ACTGCCCGCA GCTTTCGGAT 200

25 CGGCAGACCC ACCGATTTCG CCCACAATGC CTCGTTGTTG ACCTCGGCGA 250

CCAGCTCCAC CCCGGAGACC ACGGTCAGTC GGTGATTGAT GATCTTGCAC 300

TCGAAGATCG GCCCCAGCCT CGAACGCCATG ACCATTTCCCT TCTGGACAGG 350

30 CTTCACCGAG TCGACGCTGA GCAAGTCCCC CAACACAGGC AGCCGCCAGG 400

ACGGCGACGG AATCGACTCG AACTCAAGGA CTGGTTTGAC CGCGACCTCG 450

35 CTGGTGGGTG TCTCACTGCT CGGATAACGGG CACTTGTGG AAGACATGGT 500

GGACAGTCTT GCATCAGTTC CGGACTAGAT GCCGACTCGA CGCAAAATGG 550

40

45

50

55

5	GCGATGGAAC	GCAAAGCCGC	CATCCAGGAT	GGAGCAGCGC	GCCAAGAAC	600
	ATGCAAACCA	GCGCTACTTG	CGCAGACAAG	CGGAAGTCGA	ACGTGTCGTT	650
	GTTCCCCCTC	ATCTTCACTT	CCCCACTGCT	CTACGGAACC	TTCTGAGCTG	700
10	GCATTTGCA	TGATTTCCGA	GCCCCGGAAC	CAGCTATACA	GTGTTACGGC	750
	AAACCGGGAA	ACTGGAAAAC	CGTATAGACG	GCTACCCGGC	AAAACGATAT	800
15	GCTGTCTATA	CGGATAGACG	GGAAACCGGA	TGCCTGGGAA	ACTGGCTAAG	850
	TGTGTATACG	GCTAACTGGC	AAGCCGGGAA	GCTGTTTAC	AGGTAACTGT	900
	TTTTACAGCT	TTCCGGCAAA	CCGGGAAACT	GTAAAACCGG	CAAACGGGA	950
20	ACTGTAAAAC	CGGCAAACGT	TAAACAAGCG	AAAGGGCCCT	TCTCGATGAT	1000
	CATCAGTCTC	GTCAACACCA	AAGGCGGAAC	GGCCAAGACG	ACGAGCGCGA	1050
25	TCTACCTTGC	ACTCGCGTTT	CATAATCGGG	GGAGGAAGGT	TGTCGTCTC	1100
	GAATTGGATA	AACAGGGTTC	AGCAACTGAC	TGGGCTGACC	GCGCCACAGA	1150
	GGCCGGAGAT	CCACTCCCGT	TCCCAGTGCA	TGTCGTGAAC	ATGAAACGGC	1200
30	TGGTGAAGTA	CGCCACCGAT	GGCGATGACC	AGGTAGTAAT	CATCGACACC	1250
	CCGCCCGGTG	ACGGGCAAGT	TATCGACGCT	GCAATCGGGG	CGTCCAACCTT	1300
35	CGTCATAATG	CCCACGGCGG	CTACAGGACT	CGACACCGCC	AGGGTCTGGG	1350
	AGACGCTGCC	CTCGGTGCAG	GGCCGCCCTTC	CCTACGGAAT	CCTCATTACC	1400
40	TCCGCACGTC	TCGGAACGAA	CCTGCTTGAA	GATGCCAAGG	CAGCGTTCGA	1450
	CAGCAACGAC	GCAGCCCGAT	TCGACACCGT	CATCCCCATG	CGCGAGCGCA	1500
45	TCCGGTCAAC	ATTCGGTACT	ACCCCCAAGC	ACGACGAAGG	GTATTCCGAC	1550
	GTCGTCGACG	AGATCACAGA	GGCGCTGACA	GCATGAGCAT	CCCCAAGGCA	1600
	AAGACGACAC	CGACGCTCGG	GCCCCGCAAG	TCCGGGCCAC	CGATCGCGAC	1650
50	GCCCTCAGTG	ACGTCCAGCT	TCGTCGAACC	GGACGCAAGAC	CGCACGAAAC	1700
	TCACCGTCCA	GATCGACGCT	GAACTGCACC	GACGCTTCAA	AGCTGCTGTT	1750
55	GCAGGAAGCG	GCAAGAAGAT	GCGCGACGTG	GTGAGGAAA	TGATCGAGCA	1800

5	GTGGACCGAC GCGAACAGTG GTCGCTCATA ACTCGGTGAC GCTGTTACGC	1850
	AAAACCAAAG GGAGCCTCGC CGGTTGCACC CGACGAGGCT CCAGACCGGG	1900
	AAACCCCTGG AAGGAAGAAA CCCAGTCATG ACCGACTTTA GCCTTCGGGC	1950
10	AGCTCGTATT CAGCTAGGCG CATTGCTCGC CGCACTGGCA CTCGCGATCG	2000
	TCATTGCGCT CGGTATCACC ACCGGCGCAT TCGTACTTTC CTTGCCGTG	2050
15	CAACCGCGACC TTGCACGGCA AGCACTGATC CCCGAACACC TGACCTGGAT	2100
	CTTCCCGGCG ATTGTCGACA GCGCTATCCT CGGCGCCACG ATCGCCATCG	2150
20	TCATCATCAG CAAGCTCAAC ATGAACAAAGC GCGACAGAGG CTTCTACATC	2200
	GCACTCGCCG TCAGCGTTGT CGTGATCAGC ATCCTCGGAA ACGCGTACCA	2250
	CGCCTATCAC GCAGCAATCG CCGCGCAGGA GTCGATCGAT	2290

25 SEQ ID NO: 2

SEQUENCE TYPE: Nucleotide

SEQUENCE LENGTH: 1355 base pairs

STRANDEDNESS: Single

TOPOLOGY: Linear

35 PROPERTIES: Promoter

40	ATCGATCGGC CGGGATCGAC GAGTGTGCC ATTTCACCGA GCACCTCGCC	50
	ACCGCGGATC TGACGGCGCC GATCTCGGTG ATGGAGTCCT GGTGGCGCT	100
	TCCACCTGTG GTCTCGAGGT CGACGACGAC AAACGTCGTT TCGCTCAGCG	150
45	GTGTGTCCAG CTCGTCGAAG CTCAGTTGCC GCCCGACGTC GAACTTCTCC	200
	CCGTCGGAGA ACGGGGACGG AGACGGAAAT TCTCGGGCCG AGGCGGGACT	250
	CACACCGCAG ACAGTAGAAG GACCCCCGA CACGAATTG AGAGTGCATA	300
50	CGCGGAACCC GGCTCACTCC GACTTCCATT GGGAAAGCAA CGGATTGACC	350
	CCCGACAAAAA GTACGAGAGA CGAGGATCAC ACTTGCAGTG GGAACCTCGCG	400
55	AATGCGGACT CCTACCTACT TACCGGTAGG GCGATTGCGT AGGGTGTG	450

5	TACGGCGATC	AGTCGCCGAA	ACCGCCTGAT	TGATCGAAAC	GGGTTCTAGT	500
10	TTCAAGTAAT	CGGCCTTGAA	CTGCATGGAA	GATCGGATTG	TCGGGTTGG	550
15	TGACCCCTTGC	CAGTGGGTAG	CAAGCGCAGG	TTTGCAGGCC	AGGTGAGCCT	600
20	CGCCGAACAG	ACCTGTTGTT	ATCTCTTCGT	GACCCGTCCG	GCGTATCGCG	650
25	GGCGCGGCAG	CATGATTTC	GGCGAATCGG	GCGCGATTGT	CACGAAGCGG	700
30	TCGACATCGT	CGCGATCATT	TCGTAACCTT	CCTGAGACCT	AACGAAGTCT	750
35	TGCCGGACCA	AACAGGACCG	GCATCGTCAG	GAACCGCCTA	ATCGGGATCT	800
40	CCCGCAGGAA	CCCGAACCGG	GAACCCAAGT	TTCCACTGGG	GTGAATCCCG	850
45	CCTGGGGTGC	AGCACCGATG	ATCGCTGCCG	ACCACGCCGG	TAGGGCTGAT	900
50	CTTCCCAGCC	CGAACCCGTC	AGCTAACTCG	GTGGCGGAT	GAATGGAAGA	950
55	AATGGAGCAC	CCCTTAAGTG	GCGTCACAGA	GTTCAGACCG	TTCAGCGCAG	1000
60	TTGGCAGTAG	CCGGCGCGCT	CGCAGTCGGA	GCATTTGCTG	CAACCGCTGC	1050
65	ACCTGCCTCG	GCAGACCCCA	TCACCATCCC	CGCGTCGGC	ACCTTCGAGG	1100
70	TTCCGGGCGC	TTCTATTCCCT	CAGTTGCCGG	TCATCCCAGG	CATCACCGAC	1150
75	ATCGCACCGG	CCGCTCCGGC	CGCTCCCATC	TCCAGTGTG	GTGAGCAGGC	1200
80	AGTCGCGCC	GCAGAGAGCA	AGCTGGGCTC	CCCGTACGTG	TACGGCGCAT	1250
85	CGGGCCCGGA	CGCATTGAC	TGCTCCGGTC	TGGTCCAGTG	GGCATACAAG	1300
90	CAGGCTGGTC	TGAACCTGCC	TCGCACGAGC	TACGACCAGG	CCGCAGCCTA	1350
95	AATTT					
100	1355					

SEQ ID NO: 3

SEQUENCE TYPE: Nucleotide

SEQUENCE LENGTH: 2806 base pairs

STRANDEDNESS: Single

TOPOLOGY: Linear

PROPERTIES: operon

5	AGATGCCACT	GCGCCATTCC	TGGTGAGGTA	CGTCGGCCGA	CCACCGTTCG	50
	GCTGGCGTAC	CACATCCACT	TTCAAGTCCT	GCACATCCGC	ACCTTTTTA	100
10	AATGCCAAC	TATCGCTATC	ATCGTTATAT	GACGATAAAAT	AAAGAGTCGG	150
	GGTGCCTCGC	CGCAACCGGC	AGCGGGTCCA	GCTTGGATGC	GGCAGTGGCC	200
15	CTGTTCCACA	GTCTCTCGGA	CGGCACCCGA	TTGTCGATCG	TGCGCCGTCT	250
	CGCCGAAGGA	GAGGCACGGG	TTGCGGATTT	GATCGCGAA	CTCGGCCTCG	300
20	CCCAGTCGAC	GGTGTCCGCA	CATGTCGAT	GCCTACGTGA	TTGCGGTTTG	350
	GTCGACGGCA	GACCGGAAGG	TCGGCAGGTG	TTCTACTCGC	TGGCCCGGCC	400
25	GGAATTGATG	GACCTACTCG	CCTCGGCGGA	GACGCTCCTT	GCCGCGACAG	450
	GGAACCGCGGT	TGCCCTGTGC	CCGAATTACG	GCACCGACAT	CGGAGATAGC	500
30	CGTGAGTGAC	GCGTGC GGCT	GC GGCCACGA	CGAACCCCGT	GCCGAGGGCG	550
	AGGAAGAAC	CGGGCCCGAA	AAGTGGTGGC	AGGTTACCGA	GATCCGGGCG	600
35	GCTGCAGCTG	CGGGCGTGCT	GCTGATCGCG	GCCCTGACAG	TCGGGCTGGC	650
	CGGCGGACCT	GATGCGCTCG	GGATCGGCCT	CGAACGGGCC	GCGCTGATCA	700
40	TTGCCGGCTA	CACCTCGTA	CCGTCCACCC	TCACACGCCT	GGCCAAGGGC	750
	AAAATCGGGG	TCGGCACCCCT	GATGACGATC	GCGGCCGTG	GCGCGGTACT	800
45	GCTCGGCGAG	GTCGGCGAAG	CAGCCATGCT	CGCATTCTTG	TTTGCATCA	850
	GCGAGGGACT	CGAGGGAGTAC	GCGGTACCC	GCACCCGCCG	TGGCCTGCGC	900
50	GCGTTACTGT	CCCTGGTCCC	GGACACCGCG	ACAGTGCTCC	GCGACGGCCG	950
	GGAGGAAACC	GTCCCACCCCT	CGGACCTCGA	GCTCGGTGAG	GCCATGATCG	1000
55	TCAAGCCCGG	GGAGCGGATC	GCCACCGACG	GTGTCATTG	CGCCGGCCGC	1050
	ACCGCCCTGG	ACACCTCCGC	GATCACCGGA	GAATCGGTGC	CCGTCGAAGC	1100
	CGGTCCCGGC	GACGAGGTAT	TCGCCGGTGC	GATCAACGGC	ACCGGGCGTCC	1150
	TCGAAGTCGA	GGTCACCGCA	GAGGCGCAGG	ACAATTGCT	GGCGAAGATC	1200

5	GTGCGGATCG TCGAAGCTGA GCAGTCCCGC AAGGGCGAGG CGCAACGCCT	1250
10	CGCCGACAAG ATCGCCAAAC CGCTGGTTCC GGGCGTAATG ATCGTCGCCG	1300
15	CGGTTATCGC CGCGGTCGGC AGCGTGCTCG GTGATCCGCT GGTGTGGATC	1350
20	GAACGAGCCC TGGTGGTACT GGTCGCCGCG TCCCCGTGCG CGCTGGCCAT	1400
25	CGCGATAACCC GTCACGGTCG TCGCCGCAAT CGGCGCAGCA TCCAAGCTCG	1450
30	GTGTCCTGGT CAAGGGCGGC GCAGCCCTCG AAGCGCTCGG CAGGATCCGC	1500
35	ACCATCGCAT TGGACAAGAC CGGCACCCTC ACCCGCAACC AACCCGCCGT	1550
40	GATCGACGTC GCGACCGCGA ACGGCGCCAA CCGCGGTGAC GTTCTCGCGG	1600
45	TGGCCGCAGC GTTGGAGGCA CGCAGCGAGC ACCCGCTCGC TCGCGCGATT	1650
50	CTCGCCGCCG TCGAGGACTA CACACCCGCT GATGACGCGG ACGCAGTCAT	1700
55	CGGTGCAGGC CTGACCGGCT ACATCGACGG CATCCCCGTC CGGCTCGGTC	1750
	GACCAGGCTG GATCGACCCG GGGCCACTGA CCGGGGATAT CGAACGAATG	1800
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5	ACGGCGATGA CATCTGCCGC CAGCTCCGGG TCATCATCGG TGTCCGTGGT	2500
	CGGAATGCGT CGCGGCCGGG GTGTTCTCGT CATACTCGCA GGTGCCTTGG	2550
	CTGCGGTCGC GCTGCTCCTC GACCCGGTGG CACGTGGCGC GCTGTCCGGT	2600
10	GGGCAGGTAG TCGATTCGG GGTCTTGCAA CTGCGATTGG CCTACAAACAG	2650
	CGGTGTCGCG TTCAGTCTCG GTGACCAGCT CCCCCACAGTC GTCGTTCTCG	2700
15	CCGGCACCGC TGCCCTCACC GCCCGATCG GTGTGTTCGC CTGGCGCACA	2750
	GCATCTGAGC GTCCCGTACT CCAGACCATC GGGCTGGCCG CGATCACGGC	2800
	CGGTACC	2806

20 SEQ ID NO: 4

SEQUENCE TYPE: Nucleotide

25 SEQUENCE LENGTH: 22 base pairs

STRANDEDNESS: Single

30 TOPOLOGY: Linear

PROPERTIES: Primer

CAGTCACGAC GTTGTAAAAC GA

35 SEQ ID NO: 5

SEQUENCE TYPE: Nucleotide

40 SEQUENCE LENGTH: 20 base pairs

STRANDEDNESS: Single

45 TOPOLOGY: Linear

PROPERTIES: Primer

TGCATTTGTC GTTGTGAGT

50 SEQ ID NO: 6

SEQUENCE TYPE: Nucleotide

55 SEQUENCE LENGTH: 23 base pairs

5 STRANDEDNESS: Single

10 TOPOLOGY: Linear

15 PROPERTIES: Primer

20 GATCGGCCGGG ATCCACGAGT GTT

25 SEQ ID NO: 7

30 SEQUENCE TYPE: Nucleotide

35 SEQUENCE LENGTH: 58 base pairs

40 STRANDEDNESS: Single

45 TOPOLOGY: Linear

50 PROPERTIES: Primer

55 ACCCAACACT GAGCTGTTAA CGGCCGGAGC GGCGATGCA

60 TTTTAGGTGA TGCCCGGG

65 SEQ ID NO: 8

70 SEQUENCE TYPE: Nucleotide

75 SEQUENCE LENGTH: 23 base pairs

80 STRANDEDNESS: Single

85 TOPOLOGY: Linear

90 PROPERTIES: Primer

95 TGGCCCGGCC GGAATTGATG GAC

100 SEQ ID NO: 9

105 SEQUENCE TYPE: Nucleotide

110 SEQUENCE LENGTH: 24 base pairs

115 STRANDEDNESS: Single

120 TOPOLOGY: Linear

125 PROPERTIES: Primer

GCCGACGGCC GCGATCGTGA TCAG

5 SEQ ID NO: 10

SEQUENCE TYPE: Nucleotide

10 SEQUENCE LENGTH: 23 base pairs

STRANDEDNESS: Single

15 TOPOLOGY: Linear

PROPERTIES: Primer

ATTAGAGAGT GCATATGCGG AAC

20 SEQ ID NO: 11

SEQUENCE TYPE: Nucleotide

25 SEQUENCE LENGTH: 23 base pairs

STRANDEDNESS: Single

30 TOPOLOGY: Linear

PROPERTIES: Primer

35 CCATTTCTTC CAAGCTTCCG CCG

Claims

40 1. A cloning vector pSM843 which comprises:

- (a) the rep genes, ORF81 and trbA which encode proteins involved in replication in Rhodococcus;
- (b) the gene parA having the sequence SEQ. ID. Nr. 1; and
- (c) at least one gene which encodes a genetic marker selected from the genes of the cad operon, which confer resistance to cadmium, or the genes which encode resistance to an antibiotic.

45 2. The vector according to claim 1, deposited with the number CBS 102446.

50 3. An expression vector which comprises:

- (a) the rep genes, ORF81 and trbA which encode proteins involved in replication in Rhodococcus;
- (b) the gene parA having the sequence SEQ. ID. Nr. 1;
- (c) a constitutive promoter of Rhodococcus having the sequence SEQ. ID. Nr. 2;
- (d) a multiple cloning site downstream the promoter;
- (e) at least one gene which encodes a genetic marker selected from the genes of the cad operon, which confer resistance to cadmium, or the genes which encode resistance to an antibiotic; and
- (f) contains the replication origin in E.coli, deposited with the number CBS 102445.

4. The vector according to claim 3, which comprises downstream the constitutive promoter one or more genes which encode a protein of interest.
5. The expression vector according to claim 4, wherein the proteins are selected from enzymes involved in the selective removal of organic sulfur from fossil fuels or enzymes involved in the production of L-aminoacids, enantiomorphs of chiral compounds and carboxylic acids.
- 10 6. The expression vector pSM847 according to claim 4, which comprises downstream the constitutive promoter the sox operon which encodes SoxA, SoxB and SoxC enzymes deposited with the number CBS 102447.
- 10 7. The expression vector according to claim 3, obtained by:
 - (1) construction of the cloning plasmid vector pSM843;
 - (2) isolation of a constitutive promoter of Rhodococcus; and
 - 15 (3) insertion of said constitutive promoter in the vector pSM843.
8. A microorganism transformed with the expression vector according to claims 3 to 6, wherein said microorganism is selected from Rhodococcus, Gordona and Nocardia.
- 20 9. A strain of Rhodococcus transformed with the expression vector pSM847 deposited with the number CBS 102447.
10. A process for the production of homologous or heterologous proteins of interest which comprises cultivating, under suitable conditions, a microorganism transformed with the expression vector according to claims 3 to 6.
- 25 11. The process according to claim 10, wherein the protein is selected from enzymes involved in the selective removal of organic sulfur from fossil fuels and in the production of L-aminoacids, enantiomorphs of chiral compounds and carboxylic acids.
12. The process according to claim 11, wherein the proteins are Sox enzymes and the strain is Rhodococcus SMV114 CBS 102447.
- 30 13. A process for the removal of organic sulfur from fossil fuels characterized in that it uses a microorganism selected from Rhodococcus, Gordona and Nocardia transformed with the expression vector CBS 102445 containing the sox operon downstream the constitutive promoter.
- 35 14. The process according to claim 13, wherein the microorganism is Rhodococcus SMV114 CBS 102447.
15. A research method for promoters in microorganisms capable of integrating at random fragments of foreign DNA in its chromosome without requiring a sequence homology higher than 3 bp between the donor DNA and that of the host, which consists in:
 - (i) transforming said microorganism directly with a gene reporter without its promoter or with a multicopy plasmid of E.coli containing said gene and linearized upstream the gene reporter;
 - (ii) selecting the clones which express said gene, i.e. the clones which have integrated the gene reporter in their chromosome, downstream a promoter sequence;
 - 45 (iii) digesting the chromosomal DNA of the clones selected with restriction enzymes which cut upstream and downstream the gene;
 - (iv) amplifying the DNA obtained in step (iii); and
 - (v) sequencing the promoter upstream the gene reporter.
- 50 16. The method according to claim 15, wherein the microorganism is a strain of Rhodococcus.
17. The method according to claim 15, wherein the gene reporter is selected from those which encode resistance to antibiotics, heavy metals or enzymes such as XylE or Sox proteins.
- 55 18. A constitutive promoter of Rhodococcus characterized by the sequence SEQ. ID. Nr. 2.

Fig.1

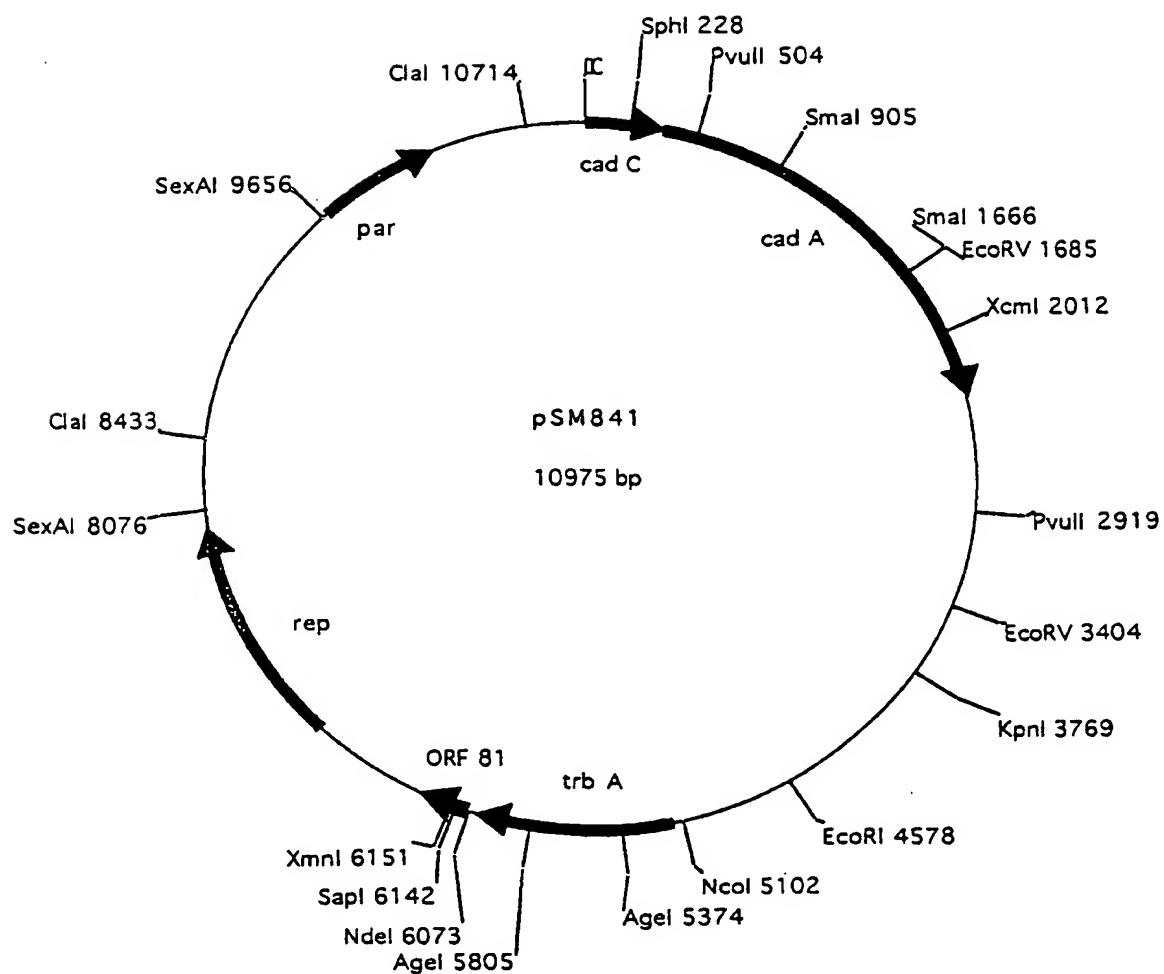


Fig.2

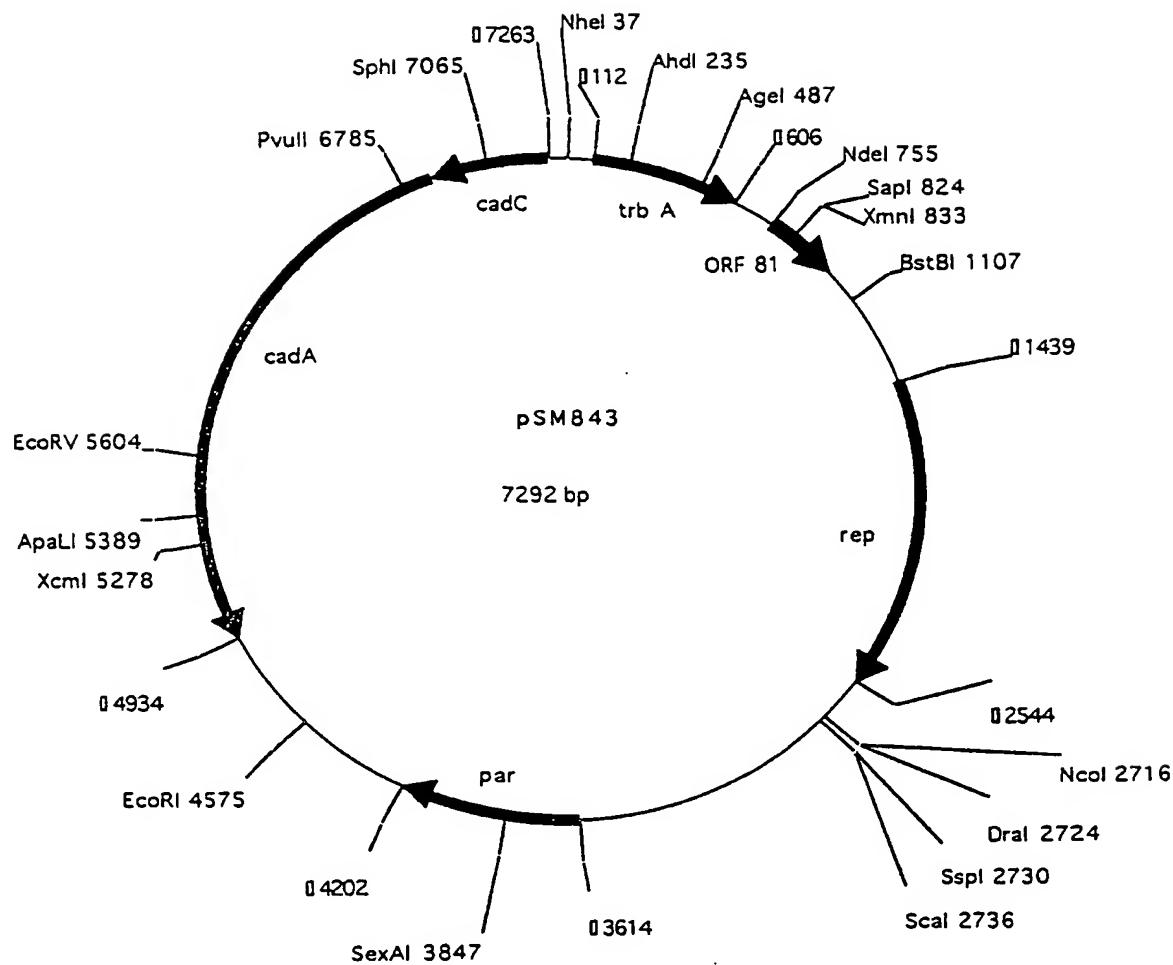


Fig.3

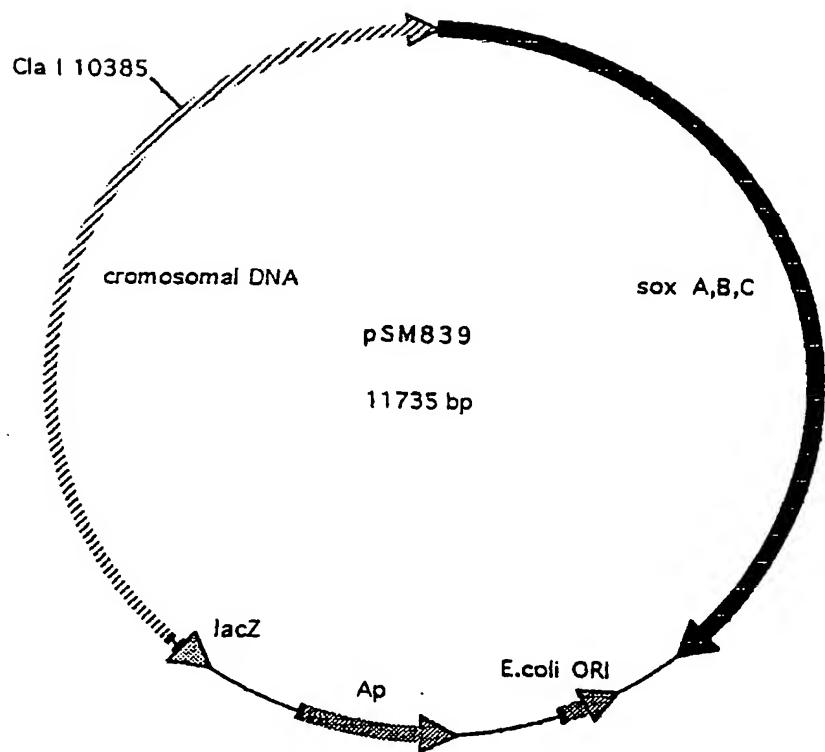


Fig.4

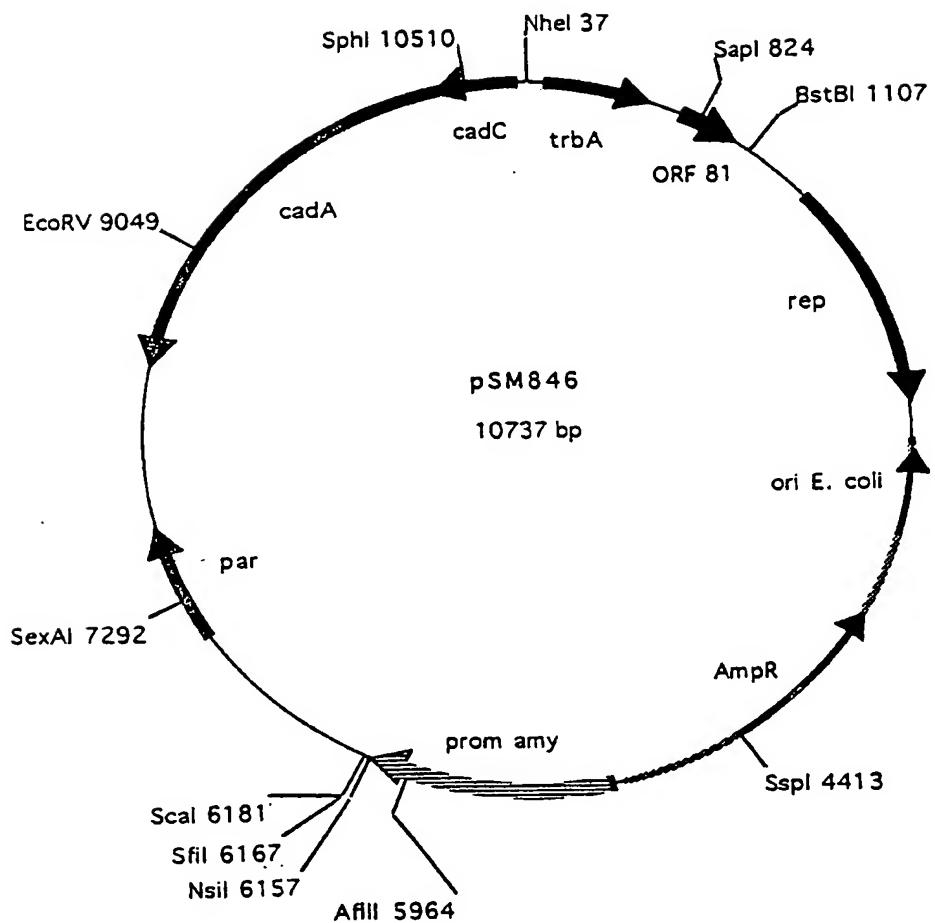
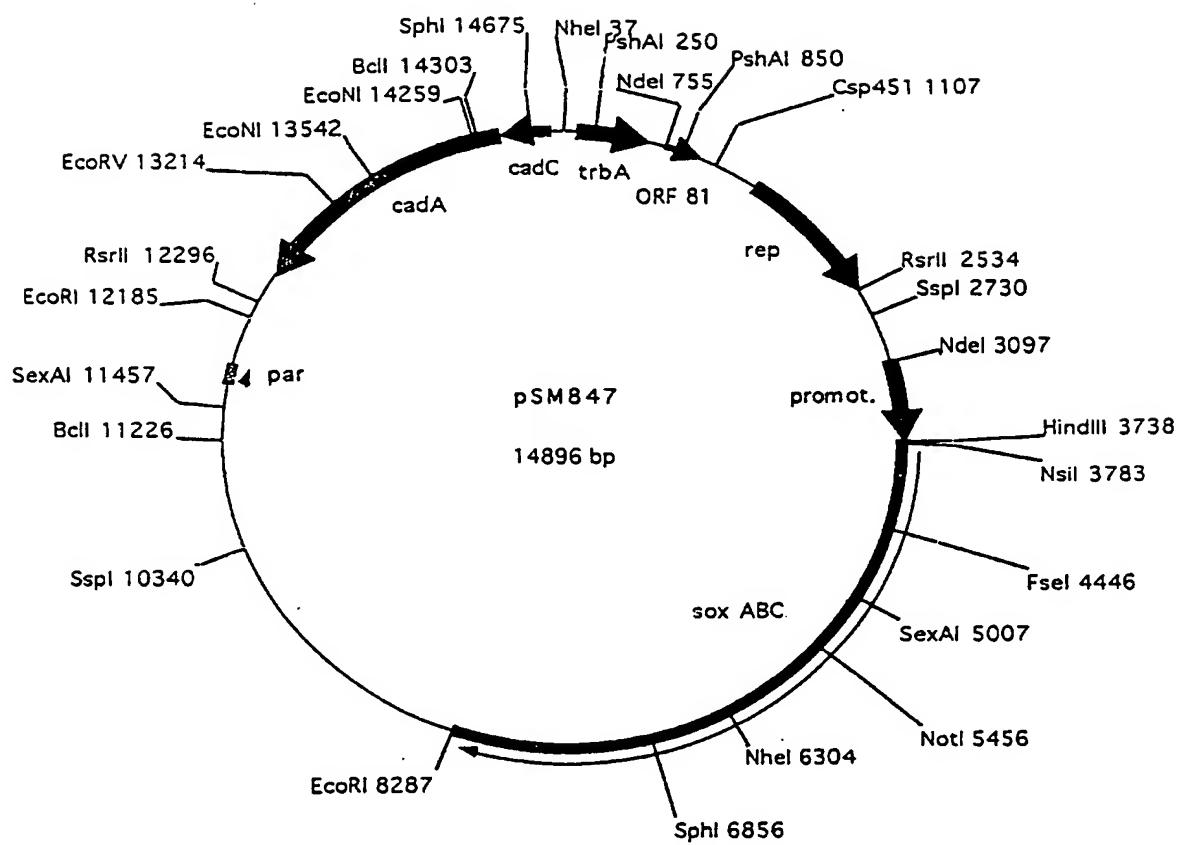


Fig.5

(19)



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(11)

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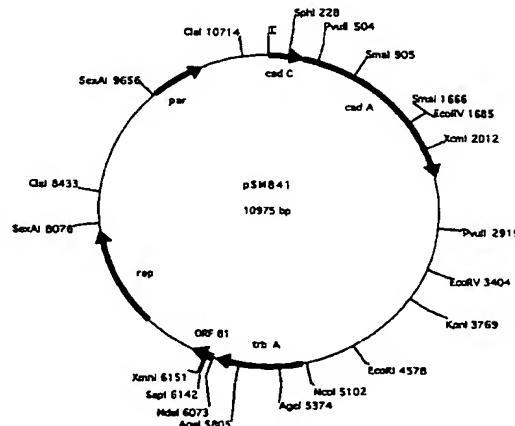
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(54) Means and methods for the expression of homologous and heterologous proteins in strains of *Rhodococcus*

(57) A description follows of a plasmid vector of *Rhodococcus*, a new constitutive promoter, an expression vector containing said promoter and microorganisms transformed with the expression vector. The ex-

pression vector has a high stability in the absence of selective pressure in the transformed strains of *Rhodococcus* and is particularly useful for the production of proteins of interest.

Fig.1





European Patent
Office

EUROPEAN SEARCH REPORT

Application Number

EP 01 20 0582

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (Int.Cl.7)						
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim							
A	<p>DE MOT RENE ET AL: "Structural analysis of the 6 kb cryptic plasmid pFAJ2600 from <i>Rhodococcus erythropolis</i> NI86/21 and construction of <i>Escherichia coli</i>-<i>Rhodococcus</i> shuttle vectors." <i>MICROBIOLOGY (READING)</i>, vol. 143, no. 10, 1997, pages 3137-3147, XP001015207 ISSN: 1350-0872 * the whole document *</p> <p>---</p> <p>WO 98 17787 A (ENERGY BIOSYSTEMS CORP) 30 April 1998 (1998-04-30) * abstract * * examples *</p> <p>-----</p>	18	C12N15/74 C10G32/00						
A		1-18							
			TECHNICAL FIELDS SEARCHED (Int.Cl.7)						
			C12N C10G						
<p>The present search report has been drawn up for all claims</p> <table border="1" style="width: 100%; border-collapse: collapse;"> <tr> <td style="width: 33%;">Place of search</td> <td style="width: 33%;">Date of completion of the search</td> <td style="width: 34%;">Examiner</td> </tr> <tr> <td>BERLIN</td> <td>27 July 2001</td> <td>Panzica, G</td> </tr> </table> <p>CATEGORY OF CITED DOCUMENTS</p> <p>X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document</p> <p>T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons B : member of the same patent family, corresponding document</p>				Place of search	Date of completion of the search	Examiner	BERLIN	27 July 2001	Panzica, G
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ANNEX TO THE EUROPEAN SEARCH REPORT
ON EUROPEAN PATENT APPLICATION NO.

EP 01 20 0582

This annex lists the patent family members relating to the patent documents cited in the above-mentioned European search report.
The members are as contained in the European Patent Office EDP file on
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27-07-2001

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